

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCTCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDIRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
GTTCCCTCTTTGCGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAACCTGAAAACCTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCCTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTTCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGTCTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPVRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTCCTAACGGACTG
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACCCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGN LGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPPYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNF FRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAGCCCATTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTTCCTGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGTGTTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACCTTGTGAATGTT
AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGILLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTNLMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCCGTGCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAACCAGCAAATCCACCCGTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCCTGAGAACTTACCTGAGATTTCTGTACAGAAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCCTGTGGATCCCCGCCCGGAAGGAG
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCAGG
 CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCACTCTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTTGAAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCAGGA
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTTACCCCCAGCCGGGCCGTGCGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGCGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCCTCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTCAGCACCGGCAACCGCCAAGTGGCCCAGGCT
 CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GGCCGTCACTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC
 CTGGCCGCCCCGACAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGGCCCT
 CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSEGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKEAWGHDELKPVSRSEFWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFREL SRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCAACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGGCCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCCTGCCTTCCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC
AGGCCTGTGGGTAGTGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGGFFSLLWLQLSCSGDVARAVR
GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDKQRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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GGGACCCATATCGGCGCGTGTACCCCCGGCTCCCTAGAGGCCAGCGCGAGCCGAGCGGACAAAG
GAGCATGTCCGCGCCGGGAAGGCCCGTCTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
GCCCCGCGCCGCGCTCCTGCCCGCCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG
CTCGCCCCCGCAGGCCCGGCCCGCAGC**ATGG**AGCCACCCGGACGCCGGCGGGGCGCGCGCA
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG
GCGGCGGCGCGCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC
AGGGCGGCGGCGCGCGCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT
GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGACTGTCATCTCTAAAAAGATTGGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCAATCTGGTTC
GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG
TCATTACGGTCTTTTGAATTCCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT
CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCTT
GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT
TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAGAACATGATTCACAAC
TGCTCCTTGATTGCAAGTGCCCTAACCATTCTAATATTCAGGCTGGATCTACTGGAAATTG
GGGCTGTCATGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT
TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAAATGATGTCACTAGAGTTCTTTAT
ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC
TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA
TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCGCAGAGGGAAGC
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG
GAGCTCACGTTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCCAGAAAGTGGCAGCCTCTGATCGTACAGG
ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTTTGAGGAAGATAGGTATTATTGCTTTTGGCTACTGTTTTAAAGAAAATA
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTTGCTTTTGATTCCCTTT
CTTCACATAAAAAATATCAGAAATTACATTTTTATAACTGCAGTGGTATAAATGCAATATACT
ATTGTTACATGTGAAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTTGCTCCT
GATTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC
GCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT
ATCAAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTTAAAAAAAGTATTTCA
TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT
GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCCTAATGGAACCACATT
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAAATCTCACAG
TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCAGTCATTTTAATGGC
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPDPTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPLELPSFYMTF
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTL AGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQ MPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGFRFTKEEKSKE LGDVMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

17/249

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

CTGTCGTCGTTTGGCTTTCAGCCGCGAGTCCGCGCCACTGGGCTGCCTGAGGTGCTCTTACAGACCTGTTTC
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAAACCACCACGACGTCATCTTCGGG
CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCCTGATCA
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC
CTATGTCCAGTTCCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCCGCGAG
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCCTG
CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTGGGGGCTGGCCTTGCTGTC
TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCCCTCTACCAGTTCGATGAGAAGTATG
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
TGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGT**CTAA**GACTCTCCCAAGAGGCTCC
CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
TCGCGCTTTCCTCTGTTTTCTCTTCCCTGTCTCCCTCCCTCCACCTTTTTCTTTCTTCC
CAATTCCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCCCTTCCCTTTCCTCTTGCTGT
TTCCTTCCCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
CTTTTCTTTCTTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTCAAGCGATTCTCCTCC
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCCTGTGCGCTTTCCTATCTGCCTGT
TTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCTCCA
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCAGCCGTCCATGCCACAGCCCC
CCAAGGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT
ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
CCCCGCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGCCAGGCTTACAGAACAC
CCTGCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALECLSASIIYPTTY
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPAALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCATGCCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTC
 TTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
 CTGGCCAGCCTATGCATTTTTAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGGCACTACAGTGACCA
 AAACAGACTGAATTCCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA
 TTATTACTCACTATGACTAAGGGTCACAAATGGGGTACGTTGATGGAGAGTGATTTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTAGCCCCAACTGGAAGAATGA
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTCACTACACTTTGGCCTGAGAA
 AATAGCATGGGATTGGAGGAGGCTGGGGGAACACCCTTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATTAGGTCTTATC
 AACAGATATGGGCAAGCAAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG
 TGGTGGGTGATGCAAAGGAAAGAGGTGAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGGTTTGGTTTCCA
 TCTTGCCGAGTCTGCCGGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGCAGAGGGGAAGGGAATCTTAA
 AGAAGTCCCTGGATGCCACACTCTTCTCCTTCTCCTCTTCCCTCTCCTCAGAGGTCTCACTCGTGGTTCTTCAT
 TTCCCTGCCCTGCCCTCCATCTCCTCTGGGTGCTGGGAAAGTGAGGATTAGCTGAAGTTTTGCTTCTCGGGGCCCTG
 TCTGAATCTCCATTGCTTTCTGGGAGGACATAATTCACCTGTCTAGCTTCTTATCATCTTACATTTCCCTGTAG
 CCACTGGGACATATGTGGTGTCTCTTCTAGCTCCTGTCTCCTCCTCATGCCCTTTGCTGGGTATGGGCATGTTAG
 GGGGAAGGTCAATTGCTGTGAGAGGGGCACTGACTTTCTAATGGTGTTACCCAAGGTGAATGTTGGAGACACAGTC
 GCGATGCTGCCCAAGTCCCGGCAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCCAGGTCTCCCTGCATGGT
 ATGCAGCCCCCTCCCATGTTTCTGGCCACTTTGTCTTTCTCCTCCCGTTTGCACATCCCTTTGGAAGTGTTCCT
 GTGAGTACATGCTGGGGTCTCCCTTTCTTCCCTTGCTCAGGTGAATCTCAGCCCCCTTCTCCACCCAAAGGTTT
 ACATGGATCCTAACTACTGCCACCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCTTTACCAGGCTTC
 TCCACCCTCCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCCATGGCCCAGG
 GCCGAGTGGCTCACCTCATTGAGTGAAGGGCTGGAGCAAGCCGAGTGACTCACCTGCTGCCCTGGAATCAGCCT
 TTTCTCCTATTTAGACCTCAGCGAGGGCGAACAAGAGGCTCGCTTTGCAGCAGGAGTGGCTGAGCAGTTTGCCA
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT
 TTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCTGGGGCCGCACCTCCAGGACCTGTTCCACCGGC
 ACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCCTGTCCCCAGACA
 CCCTGTGCTCTAGTCTGTGCAGCCTGGAGGATGGGTTGTTGGGCTCCCCGGCCCGGCTGGCCTCCCAGCTGCTGG
 GCGATGAGCTGCTTCTCGCCAACTGCCCCCAGCCGGGAAAGTGCTTCCGAGCCTGGGCCCCACTGGAGGCCC
 AGGACTCACTCTACAACCTCGCCCCCTCACAGAGTCTGCTTTCCCCCGGAGGAGGAGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTCTGCCACCCTAACGGGCAGCTGGGAACGGCAGCGGCAAGCCTCTGACCTGGCCTCTTCTG
 GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTGACCCACATCATGCCTGGCAGTGGCATGCA
 TCCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCAAGTGTTGGGCTCAAGGCTCCCAGCAGAGCTCCACAGCC
 TAGAGGGCTCCTGGGAGCGCTCGCTTCTCGGTTGTGTGTTTTGCATGAAAGTGTTTGGAGAGGAGGCAGGGGCTG
 GGCTGGGGGCGCATGTCTGCCCCCACTCCCGGGGCTTGCCGGGGGTTGCCCGGGGCTCTGGGGCATGGCTACA
 GCTGTGGCAGACAGTGATGTTCTGTTCTTAAATGCCACACACACATTTCTCCTCGGATAATGTGAACCACTA
 AGGGGGTTGTGACTGGGCTGTGTGAGGGTGGGGTGGGAGGGGGCCAGCAACCCCCACCCTCCCCATGCCTCTC
 TCTTCTGCTTTTTCTTCTCACTTCCGAGTCCATGTGCAGTGCTTGATAGAATCACCCCCACCTGGAGGGGCTGG
 CTCCTGCCCTCCCGGAGCCTATGGGTTGAGCCGTCCCTCAAGGGCCCTGCCAGCTGGGCTCGTGCTGTGCTTC
 ATTACCTCTCCATCGTCTCTAAATCTTCTCTTTTTCTTAAAGACAGAAGTTTTTGGTCTGTTTTTTCAGTC
 GGATCTTCTCTTCTCTGGGAGGCTTTGGAATGATGAAAGCATGTACCCTCCACCCTTTTCTGGCCCCCTAATGG
 GGCTGGGGCCCTTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGCTGGCGCCTCACAGCCAGCCGGGCTGCCC
 ATTACGCAGAGCTCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTT
 CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGGTGGCCGGGAGTTGTGAGCTGATGCCTGCTGAGAGGCGAGGAAT
 TGTGCCAGTGAGTGACAGTCATGAGGGAGTGTCTCTTCTGGGGAGGAAAGAAGGTAGAGCCTTTCTGTCTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCCGCCAGCCAGGGTGTTAATGCCACGTAGTGGAGGCCTCTGGCAG
 ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTTTATGGTTGTGGGAAGGGTGGGTGGCTTTAGAATTAAGGGC
 CTTGTAGGCTTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGAGCCAACGGGCACAAGCATTCTATATATAAGT
 GGCTCATTAGGTGTTTATTTGTTCTATTTAAGAATTTGTTTTATTAAATTAATATAAAAATCTTTGTAAATCTC
 TAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPF SHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
GGCACCCCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
AAGCCTACA**ATG**TTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACTCTTTCCAA
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAAGGAAAAC
GGATTTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC
TCCACTTCGTACTTCTGTAT**AGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAAATTATTCACCAAAAAATTCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
TCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSSENF TWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLTVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTGCGAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC
 TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCCTTCGTGCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTAAT
 TGGCATTGCTTGTTTTTTTGAAGTGAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTTTGTGTTGTTGTTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAAATTTGAAATATTTTAAATTGTTTTTGAAGTTTTTGTGTAAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACTTTCTTGAATTTAGA
 AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCACAA
 CCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPVSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTCTGGCGGGAGCACCCAGTCCTGTACGCC
AAGGAACTGGTCCTGGGGGCACCATGGTTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG
GGCCCATCACCCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC
GTGGACCAGAGTGACCGGGCCGGGGGCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCCCGAGGAAGCCCTGGATTTCCTCCCGCAGCTCCAGGCCGACATCTTGGCCG
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG
GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGCAGCAGTGTCCACCCCAG
TGTCTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTCTGGGGCCCCCAAGTGGTCACCTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA
GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
GATCAGGTTGAATGAATGGAACCTCTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGGCTGGGGAAGGGTTTCTGACG
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCCTGTTGCTCACACATTGTCTGGCAGCCTG
TGTCCACAATATTCGTCAAGTCCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCGGGCCTGAAAAAAAAAAAA
AAGA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLLLLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLLAQEAQGPVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

[illegible][illegible]

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWQGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSGGSSSGGSSSGSGSGSGSGSGSGSSG
 GSSTGSSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
 GGSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG
TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTTCTGAACAAGC
TGCTGCTACTTGTCTGTCTCTGGGCTGGCTTTTTCCAGATTCCCACAGTCCCTGAGGACTTGTTCCTTTCTGGAAGAGG
GTCCCTCATATGCCTTGTGAGGTGGACACAGATAGCCCTCAGAGCATGGCTTGGACAATGCGCTGTGGTGGACCCAGC
AGCTGCTCTACACCTGTGTCCTTACATCGGAGAGCTCCGGAAATGCTCGCTTCGTGGGTGTGAGGCAGTAGTG
GACGGAGTGGGGGCTTCATGAGGAAATCACCCCCACCATTACCACCAGCCTGGGAGCCAGCCTTCCAGAGCA
GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCCTTTTTCCACAACCAGCCGCCCTCCTTGCGCCGACCGTAGAG
TCGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAG
CAGACTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGACGCCCTTCTGAGCAGTGCAGAGAACATTGCTGTGGGG
TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGACGCAACATCACAGCATGATCAGGAGGGAGGTGAAAGCAGCAG
TGAGTCGCACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGGAGCGGAGGGGCTGCTCCCGCGCTGAC
GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCGAGGCATCTGGAACAGCTCCTAGGC
CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
GAGTTAGCTTCCCTCTCTCGTTGCAGATCAAATCCTATCCTAGGGCCCCCGGCACAGGTACAGGCTGGAGAGAGGG
CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCTTCTGTGGAAGGAAGACTTTCAGGGGCCGGTTCCTGCTGACGTG
CTGCTGAGGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGAGTGGGACTTGCTGCTATTCTTGCTA
CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCCTGCCTGGGCAGCCTCCACCAGGCCAG
TGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC
CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
CTGCCCTGGGCATTGCACCAGAACCTTGACCCCCGCCCTCAGGAGGAGGCCAAGTGCCCAATGCAGACCTCAC
TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCTGGCATCCACCACCGCA
ATCTTAGAGTAAGGAGAGATTGGCCGTGATTTGGGATTATGGCAGAAAAGTGCAGAGATGCCAGTCTCTGGAGTAGAA
GAGGTGGTGTGTTGTTTATCTCTTGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT
CATTTGCTATCCAGCATCTCTTAAAACTTTGTAGTCTTGGAATTATGACAGAGGCAAATGACTCCTGCTTAAC
TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
ATAAATGCCTAAGCAGAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCAGCTTTGAGAGGCCTGAGGTGCGGC
GACTGCTGAGGTGAGGAATCAAGACAGCCTGGCCAACTGGCAAACCCCATCTCTACTAAAAATAAAAAA
TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCCAGCTACTCAGGAGATGAGGCAGGAGACCTGCTTGAAC
CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCCTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG
AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTCAGCCCTG
TGCAGTGTAGTAACCTCTTGAGACCTCTCCCTGACCGAGGACCAAGCAGAGGCATTTAGAGCTTTTTTAGAATAAA
CTGGTTTTCTTTAAAAAAGGGGCTTTTATTAATAATCTCCCCACAGTATGGTCTGCAATCTGCCACAGCTT
TTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAATAATCTCCCCACAGTATGGTCTGCAATCTGCCACAGCTT
TGGGGCGTGTCTGTAGGAAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG
AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACGACACCCTGAGGTGCTCCTGAGATGCTG
GGTCCACCCTGAGTGGCAGCGGGAGCAGCTGTGGCCGGTGTCTCTCYTAGGCCAGTCCCTGGGGAACCTAAGCTC
GGGCCCTTCTTTGCAAAGACCGAGGATGGGTGGGTGGGGGACTCATGGGAATGGCTGAGGAGCTACGTGTG
AAGAGGGGCGCGGTTTGTGCTGCAGCGCCTGGAGCGCCTCTCTCTGAGCCTCAGTTTCCCTTTCCGTCTA
ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGGCCTCAGGAAGTGGCCTTGGACGAGCGTCAT
GTTATTTTCACAACTGTCTGCGACGTTGGCCTGGGCACGTGATGGAATGGCCCATGTCCCTCTGCTGCGTGGAC
GTCGCGGTGCGGAGTGCAGCAGCCAGAGGCGGGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCCGGGAGGG
CCTCACAGGAAGTTGGGCTCCCCGACCCACCAGGCAGGCGGGGCTCCCCGCCGCCCGCCGCCACCACCGTCCAGG
GCCCGGTAGACAAAGTGAAGTCGCGCTTGGGCTCGTGCAGCAGGTAGCCCTTGATGCAGTGCGGCAGCGCG
TCGTCCGCGAGCTGGAAGTGCAGCGCCGCTCCACCAGCAGCAACAGCGCGGTGCGCCT

FIGURE 32

MCFLNKL L L L L L A V L G W L F Q I P T V P E D L F F L E E G P S Y A F E V D T V A P E H G L D N A P V V D Q Q L L Y T C
C P Y I G E L R K L L A S W V S G S S G R S G G F M R K I T P T T T T S L G A Q P S Q T S Q G L Q A Q L A Q A F F H N Q P P
S L R R T V E F V A E R I G S N C V K H I K A T L V A D L V R Q A E S L L Q E Q L V T Q G E E G G D P A Q L L E I L C S Q L
C P H G A Q A L A L G R E F C Q R K S P G A V R A L L P E E T P A A V L S S A E N I A V G L A T E K A C A W L S A N I T A L
I R R E V K A A V S R T L R A Q G P E P A A R G E R R G C S R A

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTCAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGTGGCCCATTC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTTCATCACCCGAGAAAAGGGTCTTCTCATCGTGGGGCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCTAG
 AGGAGAAGCAGCCTCCGCCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAACTCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTTG
 CCCCCTCAATTTCCAGCACCCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAAATTTGTGGGGTTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG
 CACCCTTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCCTACAA
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCCTCCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTGC
 GAAAACCTCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTTCTGCCCT
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTCCTGGGATGGCTGTGCGGAGCTGT
 ATCACTGGGTTCTGTCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSASFVILFALITILILYSSNSANEVFHYGSLRGRSRPVLKKWSITDGYVPIL
GNKTLPSRCHQCIVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIABELCDHVHVYGMVPPNYCSQRPRLQRMPIH
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

[illegible][illegible]

FIGURE 36

MLRGTMTAWRGMRPEVTLACLILLATAGCFADLNEVPQVTVQVPASTVQKPGGTVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSTGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVTSGSSDRLRVRRSTAEAAARIIPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKGQAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYYRPTDSDNDSYKKDMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLLPPTLAPPQPPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAWKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLPDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHS
 PPCCCLGLVPVEEVDS PDSCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRV SFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELL SRXWSEEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLC

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AAGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG
 TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTCTT
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
 GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTACAGCATGTGTTCTTTCTGCAGTG
 GTTCTTATCACCACTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
 CACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA
 GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTG
 TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGH DVEAYCLLCECRYEERSTTTIKV IIV IYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSM AAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

ACGGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCGCGACCCAAGTGAGGGGGCCCCGTGTTGGGGTCCTCCC
 TCCCTTTGCATTCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCCCTCGCCGGGAGATGGCCCGCGTTGATG
 CGGAGCAAGGATTCGTCTGTGCTGCCTCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCCTGTCAGGCCGCCAATCGATCTGCG
 GCGATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTGCGGAGA
 AAAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTGAAGATGCACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGTTTTGCTGTGCTCGTCATTTCTGGACCAAATCTGCAAA
 CCGATGCTCCATCAGGGGGAAGTCTGTACCACCAACGCAAGAAGGGTTCTCATGGGCTGGAATTTTTCCAGCGT
 TGCAGCTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAGAGTGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAAAATTGATCACCATTGAGGAACATCATCAATTGCGAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
 AAAGGGAGAAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTTTCCATTATG
 CAACTTGTCTATGTAAATAATGTACACAGTTTGTGGAAAAATGCTATTATTAGAGAGAACAAGCACAGATGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAACATGGAGCATTGTTAATTTACAACAGAAAAAT
 TACCTTTTGATTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TTCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
 TTCGATTTACGGAATTGACAGTATATCTCTCTTATCCATATGTGATTCTGCTCGATGCATTATATTTTCCA
 AACTATACCCATAAATGTGACTAGTAAATCTTTACACAGAGCAAGTTTTCACAGATGGCAAAAAAATTTAAA
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
 GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAATTGGGAAAACTTTTTCTGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGTCTAT
 CATAATTTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCGCTACTACTCCTCAAATTATTTATTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTCAAAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCAAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTTGAACCACTTTTACTACTTTTTTTAACTT
 AACTCAGTTCTAAATACTTTTGTCTGGAGCACAAAACAATAAAGGTTATCTTATAGTCGTGACTTTTAACTTTT
 TAGACCACAATCTACTTTTGTAGTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
 AGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCAACTTCCCACATATATTTACTAAGATGATTAAGACTTA
 CATTTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATATTTACAAT
 TTGGTTTTCTGCAATATTTTCTTATGTCCACCCTTTTAAAAATTATTATTTGAAGTAATTTATTTACAGGAAATG
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATTTGCAGCTATTGAC
 TTGTGAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

1000
900
800
700
600
500
400
300
200
100
0
100
200
300
400
500
600
700
800
900
1000

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT
CCTGGTTTTGGAGTCCTTTTCCCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC
AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
TGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGT**TAAA**AAAGCAGCCCTTTTGCTTTTTTGT
TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC
TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPTKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCCTGGCCGCCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAAGTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCTCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNGSSHSGAPGPDPTLARGHNVIN VIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRRGGEYS DQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG
TGCCCTCCATGCTGTGCCTGGTGGCCAACCTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTTCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA
GGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCAGATTCAATTGATTCCCACACACCCCCCTCTCC
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTTGCTGACCTAT
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGTCCCTGCTGG
GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCT**TAGA**AGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT
GACAGCGAGATGCAAGCAAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
GCGGGTGAACAACTGCCCCACTAACCCAGACTGGAAAACCCAGAAAGATGGGCCCTTCCATGAAT
GCTTCATTCCAGAGGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFFSLGI
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGS DILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITS LIYPVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIP LFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA
 TCTCCACCGAGAGTC**ATG**GCCCCATTGGCCCTGCACCTCCTCGTCCCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGCTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGGCCACCAAGGTGTTCCCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCCGACGCGGCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACA
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA
 AA

FIGURE 50

MAPLALHLLVLPILLSLVLASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR
AHSCLSDRQLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWRREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGGACACTCTGGGCCGGCCTTCTGCCTGC**AT**
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACCTCAGAGCCGGGAAGCCCCCATTTACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTT
GCTGCTGTTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGGCGTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCT
CTGTCTCTTGCATAAAGGTTATAAATCATCACCAGACCAGTTTGTGGCATCTTTGCTCAGAATAGGCCAGAGTG
GATCATCTCCGAATTGGCTTGTACACGTAATCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT
AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA
GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCA
AAAACCTGTGCCTCCTAGCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGTGCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCTT
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTGTAATTGTCAGTGGAGC
TGCCCCCATGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTACTTCCCTC
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGGCCCTGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAATACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGTGGCTG
GCTTACACAGGAGACATTGGTTCGCTGGCTCCCGAATGGAACCTCTGAAGATCATCGACCGTAAAAAGAATTTT
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCATGTTACA
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTACTTCCCTC
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGGCCCACTG
TGCATCTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTTCTCCTATTTTTTTTTTAACC
TGTTAAACTCTAAAGCCATAGCTTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAATAAATCA
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
GATCCCAGTTTATGTTCTGTGTCCTTCCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCCTCTGTGCTTCTTCTTTGTTTTGTGATAAACATAAATTGCCAACAGTCTCTATGCTTATTTACA
TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTCTGAAAACTGCTTACAATTATGTTTTCTAGCCACTCCAC
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
CTGCGTAAATTAAATTGTTACTGAAGGGAAAAGTTTGATCATACCAAACATTTCTTAACTCTCTAGTTAGATA
TCTGACTTGGGAGTATTAATAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTTATTTA
CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
GGTGGGCCCAGTGAACTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACTCCTGAACTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATT
AGAGTTCCTGCTTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC
TATTACAGATAAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQERGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCEHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGVFFQGDIRLLADDMKTLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKEHQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEADVADMYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNI FKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVRVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG
 CCCGGGGCCCCCTAAGCCATTCTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGGCCGTGCTTTTCTCTGCTGGTGAAGTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGTGTGTTTGAACAGTACTCACCTCATGAGGATGAGGCCATGGTGTCTATTCT
 CAACATGGTAGCGCCCCGGCCGAGTGTCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC
 TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGGCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCTATTGCAG
 GGAACCGACCCAATTACCTGTACAGGATGTCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTTCCGGAGGCCAAGTTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCCTGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
 ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTTAAAC
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTTCTGAGTT
 AAAAGTCTATTTATTTACTTCCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAAACAGGCCGAACCTGGAGGGCCTGGATTTT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCCATGGACAGGCCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA
 GACTGTGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLELLVTIVVNIKLILDTR
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
 REQGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
 DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
 AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
 RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY
 KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
 EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS
 RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKEAYEVEVHRLLEAEVLDHS
 KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVDVRGNHRGLWRLFRKKNH
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAACCACCACAC
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAA**ATG**GATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
 GTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCACTGTCGCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTTGAGGGAAAACACCACCAAGCAAGTGAACACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT
 GGTTCTGGGTGTCCTCATCCCTCTCATCTGTCTAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC
 CTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC
 TCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTAAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATATTTCTCTTAACCCTATTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGAAGTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTTTT
 AACATGGTTCCCAACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAAT
 ACCTGTCTCCACATTCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAATTTTAAAGTGAATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAATGTATGGTTGTCCTTTTTTTTTGTTTTT
 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT
 GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTGTCCTA
 TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCTGCTTTTTCTTTGCTTTTCTTCTAACTTT
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT
 CTTATCAGGACAACCACCTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATTCTTTATCCCTT
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAA
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATA
 ATTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTAT
 TATTAATTTATTTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG
 ATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACCTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA
TAACATCACCCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAA
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACAGGGCCGAAGAGATGACTA
TAAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALETSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW
 MASRFSRVVLVLIDALRFDAQPPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
 VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLF
 PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHP
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAAFLYSPTAVFPST
 PPEEPEVIPQVSLVPTLALLLGLPIPFNGIENVMAELFSGGEDSQPHSSALAAQASALHLNAQ
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPCPLLLTPVAWGLVGAIA
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA
 VFFSDSFVVAEARATPFLGSLFILLVVLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLVP
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
 EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
 LLHLLAAGIPVTTGPFPTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHA AFVGFPEGHGS
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQQPPGNEADARVRPEEEEEEP
 LMEMRLRDAPQH FYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFI FEAVG
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG
 CAAACGTTACAGTACTCATAACCCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
 AACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG
 TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISSVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGAYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGAG**CCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAGAAAAAAGAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAC TGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCCTCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACTGGCCGTGGCGGAGGAACTGGCGGATGTT
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCCGAGGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCCAGAT**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGCTGAGGGCTTCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGCTGCTACAGGACCTGGGA
 TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTTGGTAGC
 TGAGGCTGTCATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCCTGGGTTCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCTCTAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCTGTCCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCCAGAAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAATA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAAYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
CGCCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC
AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAAT**TAG**GGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCCTCTGCCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAA
TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
CACCTGGGAAG**ATG**GCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGAAGTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCCTGACAATGCCCACCCTGGACAACATCCCGTTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAG**TGA**AGACTTGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILOQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSQVPSLVKALGFEEAESSLTKDVLTPASLWKPSSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGCGACGCGCGTGTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTGCTCATCGTTTTCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGAAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACAAGTTCGCTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCTCTCCAACCTGCATAGACAGTGTGTGCTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGCAAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTTTGATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTTCCTGCAAAGGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGGTGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCCAAATTATGCTGGTCCCTTATGTGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTATCTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTTGCAGCTTTGTGTTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTAGCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGGCTTTTTATGTGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTGGACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTACCCATACAGCTTTCTGATGAGTTAA~~AA~~AAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAAATTGAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTACTCTTTTTTTTTCAAGTGATTTAAATAGTTAATCATTTTAACCAAAGAAGATGTGTAGTGCCTTACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTTCCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAACTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACCTACTTTAGTTAACTTGGTCATCTGATTTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCTGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTATACTTACGCATCTTTTCTTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATGGAACCATTTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTTCTCCTCCTCTTGCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTATCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAAGATTTAGATTCAATTCCATCTCCTTAGTTTTCTTTTAAGGTGACCCATCTGTGATAAAAAATATAGCTTAGTGCTAAAAATCAGTGTAACCTATACATGGCCTAAAAATGTTTCTACAAATTAGAGTTTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGGCCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCACGAGGTCAGGAGTTCGAGACCATCCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATATAAAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCACGAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFINFPAGKGPGRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCG**ATG**CTA
 CTGCTGTGGGTGTCGGTGGTCGCAGCCTTGGCGCTGGCGGTACTGGCCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTCTGTGAGCGACTCCTTCGATG
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG
 ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGATAATTTTAAAGGGTCTAG
 ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC
 TTACCCTTCACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTACACATCTCTTTATT
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAACTGCACTGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACATTTGTCATATACTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAAAATG
 TGGTTTCTCTTGTGGATATTTACCCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCCTGGAAATATATAGCCTATTTCGGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTCTCCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC
 AGAAATTACTTATTCTTTGGATCAGAAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG
 CTTCTGTCCACCAGTATAATAAAGAGCAGTTTTATCAAGTGGAACAAAGTATAGGACAGAAT
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
 AAATGAAACAGTTTTAATAATTACCAAGTTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC
 CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCGC
 AAAAAAATAAAAAATAAATAAATAAATTACCAATTTTTTCATTATTTTGTAGAATGTAGTG
 TATTTTAAAGATAAAATGCCAATGATTATAAATCACATATTTTCAAAAATGGTTATTATTTA
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAGGATTGAAGCAAATACTGTA
 ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAT
 AGTTGTATGTGAGCATTTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSDFGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTS¹GHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS²DGAS
ILPQLFDLSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGGAGGCCCTCCTGGGATTCATTCCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCCTACAGCCTGACAGGGT
ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GGTGGCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCC**TGA**GAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRI FAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

80/249

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCCGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGAACCCTTCACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLLCRSVS

Signal peptide:

amino acids 1-24

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLLCRSVS

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCGCGTCCCGCCGCTCCCGGCACCAGAAGTTCCTCT
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCAGGTTGCAGACCTGCTCAGAGCGCCGGGCCATCCGCAACCTCACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
 CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCACTGGAGATGGTGTCTGAGGGAGGTGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAACTACATGGGGAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC
TTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCCGCC
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC
CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGGCCCCGGGCACCCAGC
CCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
GCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTT
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG
AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC
GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKRVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

Signal peptide:

amino acids 1-18

[illegible][illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAAL EERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRP GGGGEMENTLQLIKFHLAN
RTVV DSSVFP AEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTL DTEQ
QWDTPCPRENAEAA FVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFP RRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEM RKKEEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 AAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCACTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTGAGTCCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCC
 ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCCGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
 CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG
 GACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC
 TCCCACGGCCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC
 ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
 TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAAGCAACAGAGGGTGGAAGTGAAGTTTATT
 TTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATATTGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA
 ATCAAAATTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTAAGTGAAGTAATTTCTTTGACCT
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTTCTCAAG
 GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACCTCAATAAA
 TTCTGGTTTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAG
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTATACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
 GCACTCCAGCCTGGTGAGAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLSLGGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTVPATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTCACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGGCCAGCACCAGCTCAGAATAAAGCGATTC
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

96/249

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
GGCTGGATTTACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCCCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTCAGCCT
CTCAGGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGATTGAGAAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETDRFRHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNKYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVFPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTTCQVTFPGASVTNKTVHLNVSYPQNLMTVTFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLEPWAEDSPPDQPPPASARSSVGEGELQYA
SLSFQMVKPWDSTRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTCCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVVDKDFPEDRRPRKVSPVKVTALGGGKL

EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH

MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:

Signal peptide:

amino acids 1-17

100/249

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLR CANITII EHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLGWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

106/249

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGC**
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACCTT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCC**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGAATCC
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGAGGAACCAGCACTCTCCATCCTTTAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAAGCCTG
GGGTTTGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

110/249

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGGCCCTGCACACC**ATG**GCCCCCGGGTGGGCAGGGGTTCGGCGCCGCCGTGCGCGCC
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCC
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTTC
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAAGAACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCCGCTGCAGCAGCCCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT
GGAGACCGTGCACGGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCAACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTGAAGG
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTGAGCTGCTCCTGCCCTC
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGGCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCTTCTGTG
AACACCCCCCACCCTATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGGCAAAGACTCCTACGTGGAACCTGG
CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
GCTGGACCGGCCCCACTCTGCGACCAGGAGGCCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCCGGCTTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT
GTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTT
CTAAGCCCCCTGCCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQSVIERGAFQDLKQLERLRNLNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPFCVCDCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRR
 IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL
 DKGFSCECVPGYSGLK CETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLGKNNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKKGCEVS

Signal peptide:

amino acids 1-19

115/249

FIGURE 115

CAGGCCATTTGCATCCCCTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAACTTGTACATGGCTCCC
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT
 CCATTGACCACAGTGTCACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTTCATCCGTGAACCTTCCCTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LR SFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

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FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTAC
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAAGTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTCGAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
 CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTTAAATCATTGTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTS DPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFD PDRFDDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCTCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGCGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTT**CTGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCACGGGTGC
CCACTCAGGTCAC TTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGAG**GGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

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FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCAATCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTTGTGCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

QLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

GTGAAATGTGAGGGTTTGTATGACTTTTCAGATGTCTAGGAACCAAGAGTGGGTGAGGGGCCCA
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
TGGTGGAAGTGTGCGCGCCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
CATCTTCCCGAGCACCCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
GGCTGCGGCTGCCCACACGGCTCACC**ATG**GGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
GCTCCTCTTCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGT
TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTTTGGTTCTTGTA
AAAACCTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT
TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

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FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLG
GIMSGVFSFVNTLSDSLPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKN
FLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCTCGGTTCGAGAGCCATCTGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG
 AGTTTGTAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCGTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAACGAACCTGTGTGTCAGCCCCCACCAGAATGAGTCGGAGATTGAGTTCTTCTACGTGGATG
 TGTCCACCCTGTCAACAGTCAACACCACATACCAGCTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTTCACTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
 CGGTAAATTGTCAAGGTGACCTCCAACAGGCCTTCCCTGCTCAGTCATCTCCATTGAGGATGTGCTGTGTCTG
 TCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC
 AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT
 CCCTGCCTTTCTACCCCTTCGACAGAAATGAACCGGTGATCAAGGGCACCGCCAGAAAACCTGTGAGTGTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATATTTCTCTCTTTTACC
 TGCTGACCGTCTCTGCTGGCCTGCTGGGAGAAGTGGAGGACAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
 CCTGCCAGAAAAGCGTCCACCTCGAGTCCCTGGCTGATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
 GTTACCAGGGCGCTCCTTTGAACCTGTAGGTACTCGGCCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCAATTCGCACCAAGCAATACCTCTATGTGGCTGACC
 TGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTTGCTGTCT
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
 GCTACTACAACCTCTCTGCGCCCAACCTGGGCAATCTCAGCGCCTTCAACAACATCTCAGCAACCTGGGGT
 ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA
 TGGAGGGGCTGCTCAGTGTGCTATCATGTGTGCCCCAACTATAACCAATTTCCAGTTTGACACATCGTTTATGT
 ACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG
 CCTACGCTCCTTCCATTGTCTATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTTCT
 GGATCGTCTTCTCCATCATTCACATCATCGCCACCTGCTCCTCAGCACGCGAGCTCTATTACATGGGCCGGTGG
 AACTGGACTCGGGGATCTTCCGCCGATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
 TCTACGTGGACCGCATGGTGTGCTGGTGCATGGGCAACGTCACTCAACTGGTGGTGGCTGCCTATGGGCTTATCA
 TGCGCCCCAATGATTTTCGCTTCTTCTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT
 GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCTTGCAGAGTCCAGGGAGCACA
 ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTTCG
 GGTCTTCTTGGTGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTCTAGC
 AGGAGCTGGGCCCTTCGCTTACCTCAAGGGGCCCTGAGCTCCTTTGTGTCTAGACCGGTCACTCTGTGCTGCT
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCC
 AGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTGGGGCCTCCATGGGCCCTGTCTTTGGCTCTCCATTT
 GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCTCCCCATTTTCATGCCTTGCATTTTGGCCGTCTCTCCCC
 ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG
 CCTGGGGCAGTGCATTTCTTCTTCTTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAAT
 TGAGAACCCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACCTCTTCATCCCATCAGCTCCAGACTGATGCC
 AGCACCAGGACTGGAGGGAGAAGCGCTCACCCCTTCCCTTCTTCTTCCAGGGCCTTAGTCTTGCCAAACCCC
 AGCTGGTGGCCTTTTCACTGCCATTGACACTGCCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTTTCA
 CCCGTTTCTGCCTCCACAGCTGTGGGCACCCAGTGCCTACCTTAGAAAGGGGCTTCCAGGAAGGGATGTGCTGTT
 CCCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCCAGGCA
 AGTTCTGTGTTAGTCATGCACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC
 CCTGGCCACCTGGTCTTGGATCCCTTCGTCCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGGATGGGAATGTGTTTTTCTCCCAAACTGTGTTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATGAGGTGGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT
 TGCATTCAATAAACAACCAGACTCAAAAAAAAAAAAAA

FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESH LGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
 EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
 SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
 VKVTSNKAFFPCSVISIQDVLCPVYDLDNNAFIGMYQTMKKAAITVQRKDFPSNSFYVVVV
 VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
 TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL
 VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
 ARKDKRVLRRKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYNFLCAHPLGN
 LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
 MEGLLSACYHVC PNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
 VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLY YMGRWKLD SGIFRRILHVLYTDCIRQCSG
 PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
 KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDDFFDDHDIWHFLSSIA
 MFGSFLVLLTLDDDLDTVQRDKIYVF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTG
 ACC**ATG**GTCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACCTATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
 GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGGCCAGGA
 TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC
 GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTGCGC
 AGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCTGAAGGCG
 ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPaelSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSpDMFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIIESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFfeVNAEGNLYVTRELDREAQAeyLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLsaEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAfQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTaIDADLEPAfRLMDfAIERGdTE
GTFGLDWEpDSGHVRLRLCKNLSyEAAPsHEVVVVVQSVAKLVGPGPGGATATVTVLVERV
MPPPKLDQESyEASVPISAPAGSfLLTIQPSDPISRTLRFSLVNDSEGwLCIEKfSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALTlAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRcNV
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTCAATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGCGGCCCGGCGTTTGGCTGAATGCAGGCATCCATTCCTGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACT**TAG**GCGATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
 AGCATCACCCCTTCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAGAAACATC
 TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTCT
 TCGCAGTCTTCCCTGGAAAATATTTTCTTTTGGAGCAGCAAATCTTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTTGTGTTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTTCAGGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAGGATGGTGAATTTATCCCCATCTGTCTAATGGGCTTACCTCCT
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTGGTTTTG
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
 GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCCTTTTGTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

[illegible]

FIGURE 136

MASYLYGVLFVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGMROLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGCGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCGGAGGCGGGGGCCCCGGGGCGACTCG
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC
 GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGTCAGCCGCCGCTCCGACCTGGGCGCTCAGC
 CCCCCGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGCTGAACACATCTCCAACCTAC
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
 AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
 CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTGTCTCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
 ATTCTGAGAGCCTGGGCAGCTTGCAAGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
 CTACAGCAGCGTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCCGACGATGGCTTCCCCTTCAAC
 GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
 TCCCAGTGGCACAGGGGAATACAGAAGGCTCTGCCGTCTGTGTCTTCACAATGAAGGATGTGCAGAGAGTCTTC
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
 CCTGGAGCGTGCATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCGTGCTG
 AACTTCTCAAGGACCACTTCTGATGGACGGGCAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
 TACCAGCGCTGGCTGTACACCGCTCCCTGGCCTGCACACACCTACGATGTCTCTTCTGGGCACTGGTGAC
 GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
 CAGCCCGTGCAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
 GTGCCCATGGCCAAGTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCGGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTGCAAGCACGTGAGCCTTACCAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG
 GGAGCCAGCGCCAAGGACCTTTGCAGCGCTTTCGGTTGTGTCCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
 TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
 CTCTGGCTACGCAACGGGGCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
 GTGGGCACCCAACAGCTGGGGGAGTTCAGTGCTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
 TGCCAGAGGTGGTGGAGGACGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA
 TCGCGTGTGAGTGACCAAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCCTGGTG
 ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA
 GTCTTCTGAAGCAGGGGAATGTGCCAGCTGCACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
 CCACTCAACGGCTTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
 GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
 TGCCCCCGGGCCCCGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTCGTGAAC
 ACGACCGTGGTGGCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCACCCAGACACCCAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTTGGTGGAA
 CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCCAAATGTGAAACTAGAATGAGAGGGAAGAG
 ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
 TTGTCTGAGACAGATTGGAAACCTCACCACTGGCCTCTTCACTTCCACATTATCCCGCTGCCACCGGCTGC
 CCTGTCTCACTGCAGATTACAGGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
 TTGCTGCCGTGCTCCACCACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC
 GGACCCAACCTCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
 TTTCTGTGACAATGTACGCCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCTCCGTTGTTGCGTGA
 GAACCCGTGTGCCCCTTCCACCATATCCACCCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
 CTGGTCTCTCCCACTCCCACTTACCCTCCATCCCTCACCTTCTTCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTTATGTCAATTTTTTAATAAA
 GTCTGAAGAATTACTGTTTTAAAAA

FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCF
FDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFFEFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFENVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLVLVGTQQLGFEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC
 GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGTCTGCGCGT
 TGCCGGCCCCCGCTCCCCGCGCGGAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCGCCGTAGCGCGCGC
 CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGCGGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGGGG
 CCTGCGGGCGGGCTCGGGGGCCCGATGGGCGCGGGCGGGCCCCGCGGCGGGCGGGCGCTGCCCGGGCCGGGCTCG
 CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGGCGGGCGG
 GCGGGCGGGCGGGCCCCGGGCGGGCGGAGCGGGCGGGCGGCGGCGGCGGCGGCTGGCTCAGCGAGTGC
 TGCTCGGGCTCGTCCCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCACGGCGCCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGCAGGCGGGCGGCTTCCAGGCGGGCGGGCGCGCG
 GCGATGCGCGCGGGGCGCAGCTCTGGCCCGCCGGCTCGGACCCAGATGGCGGGCCCCGCGCGACAGGAACCTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCCTACAGAACATGGTCCAAGACAA
 TTCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
 GTGTGGACGACTCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACCTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCCCTCTTCTTGGGCAGACAGGCTGGGCACCACGGAAGAAATGGGAAAACCTGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCCGAGAATGGTGCCGC
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
 ACATTAGAGATCTCATAACAGTAAAAATCACCAAGCTATCACATTACACCCCAACAAAAACCCACCCTACCAGT
 ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAATACAGCTGCACCGCGAAA
 TTGTCTGATGAGCAAATACAGCAAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCCGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTCTATGCAGGTCA
 TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA
 TGACGGTCCCTGTGAGGAGGCGACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACCTCCCTGAAGA
 AGCTCGTCCCTTTTTCAGTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAAGATAAACATACTGA
 TTCTTTTGTCTGGGCGTTTCCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAGTTGAACGTATGA
 GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCCTGGAAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTTCTGCGACGTGACCTCGTGTCTTACTA
 CAGAATTCCTTCAGCGATGTCGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAACCTGGCTTCT
 GGAGAACTATGGGTTTGGCATCACCTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
 TAATTATCTAATTTATTTTCAAAAAATTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
 AAGTGGTTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTTGCCTTTGAA
 CACATCTTCTTGTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAAACCTTT
 TTTAAAAAATGTTTTCTTTTGGAGCCCTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATTCTGCAAGATAT
 TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT
 GTTTTGTTTTTTTTTTTTACAAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
 GCTGTTTCATCATTTGTCTTCAGGAGAGCTTTCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTTTGTTTGTGTTTTGTTTCTTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
 CAGTGGCGCAATCTTGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTCCCCTGCCTTTGCCTCCCGAGT
 AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTGTATTTTGTAGTAGAGACGGGGTTTACCAT
 GCAAGCCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTTATTGGCCATAATAGACCTGGCATTAATTTCAAGAAGGATTTGGCATTTTCTCTTCTTGACCCCTT
 CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
 GAAACATACACACATACCCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTTCTTTTCATCCTGTCTG
 TGTATGTGGGTGGAGATGGTTTTTCACTTTTCACTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA
 TTTATTTAATATCTGTTGTTTCAAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGACTCTCAAAGATTTCTTTTGGAAACGCTTTTTCCCCTCC

FIGURE 143B

TTAATTTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

145/249

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFLVLAASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWFRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
TAACTCTCCAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAAATTTTGGTTCAGGAAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

CCGGCTCGAGCGGGCTCGAGTGAAGAGCCTCTCCACGGCTCTTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCC**ATG**GCTTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGG
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTTAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCTCCAGC
CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA
GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGTTGGTATGTGGGAGTGTGTGCGGGATGACGTAGACAGGGGGAAAGAACAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC
ATTCAATCCCATTTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
GAAAAGGGGACTCCCATATTTCATATGTCCAGTGTCTTGGGGAT**TGA**GACAGAGAAGACCCTG
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAG
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTGTGTTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTCCTGCCTCACAGGTGAAGATTAAAGAGA
CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGGCACAGTGTGTTGCTAATGATGTGTTTTTA
TATTATACATTTTCCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
GAGGTAGGATTTTTTCACTGATTCTATAAGCCAGCATTACCTGATACCAAACCAGGCAAAG
AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAA
TTCTAAATAAAATTTTAAACAAATTAACCTAAACAATATATTTAAAGATGATATATAACTACT
CAGTGTGGTTTTGTCCCACAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAAAT
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA
 TTAATATAGCACATTGTCATTTACAACAGCAAACTATATGCTGAGTTTGGCAGAGAGGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACCTTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAATCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTGTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACATAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCAATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCGCGGCCTGCCTGTGCCC
AGGACTCTCCAGCCCCGCCCAGCCGCCCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTTCGCTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGCCAGCCGCCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCT**TGA**
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTT
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAFPSPVLHYWLLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTL VHAAVGVGTALALLS CAALVWHFCLRD RWGCPRRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGTTACT
 TTGGAAGTTTGTCTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAACAACCTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTCTATGTCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTA**TAA**AAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATT
 FTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTT
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAA
 TCTGTATAATTTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCCTAATTTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTAGAATGATGCTGGTCTTTAGGAAGTATTAATAA
 GAAATTTTGACATAACTTAGTTGATTGATCAGAAAGGACTTGATGCTGTTTTTCTCCCAATG
 AAGACTCTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACCATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTATTAATTTTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAA
 AGAAAATTAATAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCACT
 GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTG
 CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
 CTCTGCCCCACAGCCTCAGCATTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC
 TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCCTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
 TTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCA
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACA
 CCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTCATGGAGGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC
 CTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTTCATCCGCCACGCGGTCTGTCTCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTACGCACTTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATA
 CACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCTGTACCTGGGAACCACCACAG
 GGTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGAAGAGATTAGCTGTTCCCTGACC
 CTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCAGGGTGCAGTGTGTGTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCACTGTGCCT
 GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATT
 AAGAAGTCTGGCTGTCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT
 GGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACCAGACCTTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCCTTGA
 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCT
 TTGCCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
 TTCAGGGCTGTGAGACCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC
 CAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAACATC
 TAAACAATCATATGCTAATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT
 TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC
 TTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG
 CAGGGGTAACTCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT
 TTGGGATTTCAGAAAACCTGCTTGTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

AAGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAATTTGAAAACCTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGT
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTTCTTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
 CATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCCTTGCTTTATGTTT
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
 GTTGAGGCTTGATGGAAAAACCTATTAACCAGTACCACAAGACTTGGAGAACTTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAGTGTTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
 TGTCTTTACAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCTT
 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTAGTTTCTGTTT
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
 GCGTTATCTCTCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPF
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCShWPkdVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQYLFDFVFVLLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCCGTCACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**TG**AGGACCCAAGTCTTTCAGCACAGAAT
 CCAGCCCTGACAACCTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCAAGTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCTCCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCTATTACCTGGGATTCCATGATTCATTCTT
 CAGACCCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTTTCTTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACGTATACTAAATTAATAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGP
GGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPV
RGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPFVISAFANDPDVTREAATSSVLLPLDPGDRV
SLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

[illegible]

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWLVFDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

[illegible]

FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFEVSVGLVINQVQLCTLALWPFVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMVRRFPLEDIPLEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFVGFGAASFGVRRRLIGESLEPGRWRLQ

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTCTCTTGTCTGCTTCCTGTAATGTGGTATGCCATGGGGTCTTTCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
TGCTGGTCCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHSLQCPGAATRHIHLVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR

EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGLSKYLELQEPSWS

GPCPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

170/249

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAAAATCTGTTTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
CTAACCTTTTTCATGTCTGACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACCTTGCGCAAATATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGC
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
TGAGAGGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

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FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC
CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNAL EELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

TTTGTTCTCTCCTGGATCTTACACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCCACTTTGAAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAATAGCTGTATTCCTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTTCTTAGATGAGGAAAGGACAGGCTGCTCTGGGAGCCAAAGACCACAT
CTTCTACTACAGTCTGGTTGACTTAAACAAAAATTTTAAAGAGATTTATGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTCCGATCCTCAGCAGCC
TTTTGCTTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCCAAAGATACTGCAT
CACTCGATCCCTTGGGCTACTCATGACCACCTACATCAGAACTGACATTTAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAACCTTCTCATACCCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTCTG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGAATGATGT
AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGACGAGCTTTTGAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTTAGCCCCACTGATTAAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGGAAACGACATTTGGAACCTGTCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA
AGAGGTAGTCTGCTGGAGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCA
GCAACAATTTGTACATTTGGTTCCCGAGATGGATTAGTTTTCAGCTCTCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAACTACCCAGTGTCTGGGACATCGAAGACAG
CATTAGTCATGAACTGCTGATGAAAAGGTGATTTTTGGCATTTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATCTGGGATGTATTACTG
CAAAGCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTTGAAGATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTACCGGTTGAGATACAAAGA
CTACATCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCAAAGTGGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTTAATTTAAAGAAAAGAAATTCCTTACC
TATAAAAACATATGCCTTCTGTTTTGTATATCCCTTAGATGATTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
CACAAAGCAATAATCTGAATAAGACAATATGTGTATGAATATAAGAAAGGGCAAAAAATTCATTTGAACCAGTTT
CCAAGAACAATCTTGCACAAGCAAAGTATAAGAATTATCCTAAAATAGGGGGTTTTACAGTTGTAAATGTTTTTA
TGTTTTTGAGTTTTTGGAAATTTATTGTCTGATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCTCTGAATGTCCATTAAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGGAACACGCTACCTTGTGTTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATTTATC
AACAGGAACCTTCTCAGTGAGCCATTCTACTCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTTTCT
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAGACAGCCAT
AAATTTCTGGCTTTGGGGAAAACATATATCCCCATGAAAGGAAGAACAATCACAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTTAAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATTTCTTGAAGAATCATAGGAAGAGTAGACATTTTTATTTATAACC
AATGATATTTTCAGTATATATTTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC
CTTTATTTCTCTCCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAAAC
ACGGGAAGGGTTAAATTTAACTCTTTGACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAATTT
GTAGTATTTGTTTTTGAATTTTAAACAATAAATAAGCCTGCTACATGT

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
 GSSEGLDFQTLTLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNGAKFIGTFF
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQSRSLINKWTTFLKARLIC
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
 AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
 LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCPTYGKACADCCCLARDPYCAWDGNA
 CSRYAPTSKRRARRQDVKYGDPIQTCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLTLN
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
 KGGPKWKHMQEMKKKRNRHRDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTGTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTACTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTGAGGCTACAGAGGGGGAGGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGAGAGAGCTGTTGGCCCCC
CAGGGCCACCTGAACTCTCTGACCTGAACAGATGCTGCCGTCCCTTCTCCTCCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCCTCACCTGCAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTGAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCTCACCTCCAAGGT
GGAAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTCCCATTGTTCTATCATCTCTAGGACC
GGAACACTACTCCTTCTTCTGTCTGTCATGACCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCTGGCTCCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGGTTGGGCTGGGAGAGGAACAGGCCTTGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG
CTAAGAGGGCAGGGGGCCTACGGTGCTATTGCTTTAGGGGCCACCACGGGCAGGGGCCTGCTCCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGAAGGCGGGGAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTCACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAAAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGTTTACGGGAGCCGAAAGGCTTAAATAGTTTAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCCAGTG
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGCTGGTTGCTTGGCTGCCCATTTGCCTCTTGAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
GGTCCCTGCCCCACCTCAGAGCCCCAGCTCCTGTCTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCCTGTCCGGGGCGGCTTTTCTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
CCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCAGGTGCATGTGTGATGATGGGAGGGGGCTC
CGTCTTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
TCATGTTTTGTTTTCTTACGTTCTTTACGATGCTCCTTAAACCCAGAACCCCAATTTCCCCAAGCCCCATTT
TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPSSQSDNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

FIGURE 179A

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTGCGCAATAATAATACCTCCCTTAGAAG
TTTGTTGTGAGGATTAAATAATGTAAATAAAGAAGCTAGCATTAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAGGAAA

[illegible]

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNQSVLPVPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
 GTYLTGTINGDPESVASLHWDGGALLGVLYQYRGAEHLQPLEGGTPNSAGGPGAHILRRKSP
 ASGQGPMCNCVKAPLGSPPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCAGGVQFSSRDCTRVPVRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCTGTGCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
 CTCAGAAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCCTGCGCCGTCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
GGCACCCCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC
CAGGGCCACCACGAÇCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLISLIGGTLLCLSCQ
DEAPYRPHYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 185

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCACCACCACATGCCAAGTGGTGGCGTTCTC
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTG
 GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
 TTAAGTCCTAAATATAGTTAAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
 ACTAATTCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTCTTCTGTGGCAGAGAGAACCTGCTCAAAGCAGAGAAGTAGAGTTCGG
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTG
GGCTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACCTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTG
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
TCATCCCTGTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
GTTGCCCAAAAACGTGAGCTTGAGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTG
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTTAACTTTACTATAAAGC
CATGCAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAAACTTTGATTTA
CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA
GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCTCATTTATAATGA
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTT
TTCTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
GTTTTAGGAAAGTGAAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
ACAAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAATTTG
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
TTAATAAATTTGTACATTTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA
TTGTCTTTGTTCATCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTGAAGTATTTAAATTCATTT
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCAGTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCCACCTCCGGAACCTTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCTCGTCTCACCCCTTTACACTCACATTTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLLIPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAISRGPS EYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGTCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGGCCAAAGCATAACCTTCTGGGAACTTCAGGAGTCCTCTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER

AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL

FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATG**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTTCAGTTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAAACACGTCAATAAAAAAATAATCTCCCAGA

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNQGRVQFLHDGSC

Signal peptide:

amino acids 1-19

197/249

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTTC
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
 CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTGAGGGACCCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCGGACTCCCCGCAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTCAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCCTGCCCCGCCGGGGTCCGAGCCCCGGCCCCCTCCGGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCC**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
 GGACCTTGCTCCCCGCGCCGCGGGCGGGAGCTGCTGCCTGCCCAGGCCCGCCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
 CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
 GGCCGCCCCGGGGGCCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPULLAGIHCAKRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

1
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3
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FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGC
 TGTTGGCAAATGTCAGGACCAGGTAAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT
 TGCACCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAGCCTGGACCCAC
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCCTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGAGGAAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACAGCTGCAAAGGAGACTGGGTGTGCGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGACAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTCACTTTGGCAGCCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA
 GATAAATGCTGTGGATGAACGA**TGA**ATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKA EKPCMERLQLQRRLLGCRTFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLOHTSRKEIHFGSP
QHL CFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGAC**ATGGA**
GTCCAGGATGTGGCCTGCGCTGCTGTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCACCAGCCCCAGCC
CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC
ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCCG
ATTTCTGGACTATGGTTTTGCAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGGCACCTGCCACCCTGCGGCCATT
CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAATTACCATCTCCAT
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCTTCGGGGACTCACCTACCCCCACCCC
TGACCATGAGGAGCCCCGAGGGGGACCCCGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG
CCTTCCAGTTGAACCGG**TGA**GGGCGAGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCAAC
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
CTCCCACAGCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC
CTTCTCCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCCATAACTCCAACCTGCCCC
TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC
CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT
TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
AAGCAGGAGGCCAAGGGGGCCGGCACAGCCCCCATCCCCTGAGGGTGGGGCAGCTGTGGGGA
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTTGACACCACCCGGAACACTCCCCAGCC
CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCG
GGTCCCTGTCCCCACCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
TGGTCAGCGTTTTCTGCACACTTTACCTCTCATGTGCGTTTTCCCGGCCTGATGTTGTGGTGG
TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTTCCGCAGCCCCCTGC
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTGATGG
TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA
AGGGACTCCCATTGCCCCCTCCCTTTCTCTACAGTCCCTTTTGTCTTGTCTGTCTGTCTGGCTG
TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT
CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
ATCGGGAGCTCTGCCTCCAAGTCTACCCCTCCCTTCCCGGACTCCCTCCTGTCCCCTCCTTT
CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT
CTTCCCTCCTTCTCACTGGTTTTTTCCACCTTCCCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
GTGATATATATTTTTGTATTATCTTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
GGATGTAAGTTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGTGTCGCTCGTGGTTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC
CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC
CTGGCTGTTCATCGGGTAGGGCGGGGCCGTGGGTTTCAAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAAGTAAGTCCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGGCTGCAGTCCTTTTCTCCCTCAAAG
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCTTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGGCTGACTGCCCCACATTGCCTTTTACAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTCTGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAI IER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

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FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GGAAGCTGCCCCGTCCAGGTTTCATGTTTCCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAAGTTGCTGCAGAAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGGCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAACCTAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCT**TGA**CTTCTCCTTGGAACCTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCACACACACACGACGTGCACACACGCACGCACGCGTGCACAC
 ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
 ATGGTTTTTAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSEFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMOVTEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCGAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGTCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGA CTGCCCCGGGCTGCCGCC
CCCCGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
TCTCGGCCACGGCTGGGTCTGGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
TGGCAGGTGGGCTGAGGGGGCGCGGGCCCCGGCGCAGTCCCCCGCGGGCCCCGACCCTGAGGCG
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCCGGC
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
TCAAGGATGAGGTGGGCGCACCCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAAGTAATGAAAAGAATGATTTT
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAAGTTTGAAAATTC AATTGAAT
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA
TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCTGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCCTGTTCTCATGATGTCAGG
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSFVPACSLVESHLS DQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQEOKSFFAKYWMIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSGLCCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTCGTCCGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA
ACTGTCAAGATGCCGGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCATCTTCATCTTTGTCTTCCT
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCCTGAGCTG**TAA**CCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT
GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHSDRKTGTRNMFSICSAVMVMALLAVVGLEFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTA**CTTT**CAAGTGCTGAGTCCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGG**TAG**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGT**TTT**GGGGACTCAATAAACCTCACTGACTTTT**TTT**AGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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900
800
700
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900
1000

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSiHCMDLSQRYCLMAVFNVIYLENEDESE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTCACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

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FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAG**GAT**GGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATAACCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTTCAAGTGGACCCAGTGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTTTCCATAAAATCATCGCGGGCAGCGTGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC
 TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCCCTTGTCCGTTTTAGTGCATTCATAATACTGGTCATTTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTTAAATATA
 TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTCGCATTTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAA

FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPT VLLTMLS SAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLR TIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKE LHLEHNQFSKLN LALFPRLVSLQNL YLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADA EHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRY PASKMLQQRSLMRRHRKKKRQSLKQMT PSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA

ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP

VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTA
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC
ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAACT
CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTTCAAGTCTTGATTGTGGC
TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA
CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTGGACTCATT
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
ACACAGTGGATGTGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
GCTGTCCTTCTGGATGACATTTTGAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC
TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
TTTGTATAAATCTTTTGTGTTTGAAGTCAAGCTGAAATGAAAACACTGAAAACATGGATTCT
ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
TCATTCTGTCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG
CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA
AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT
GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT
ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
CTCTATAGTAAGTGCCTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCCGGGCCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA
CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
CACAACTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACCAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
TGCGCTACCTGAGCCTGGATGGGAACCCCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCCAG
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCCTGGACCTGTCCGGGCAACCCCAAGCTTAACT
GGGCAGGAGCTGAGGTGTTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGGCCCCACC
ATCTT**TGA**CAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTTGGGCTGCCTCAG
GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
AACCAGACTCGGGTCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT
GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCCCTGCTGCAGGGCAGA
GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCCAGTCACTCAGGGGCGAGTT
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCTTCTCATGTGAC
AGATGGGGAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCCTGCGGGCAGTGGC
ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCCGACCCAATGCACTTTCTTGTCTCCTCTA
ATAAGCCCCACCTCCCCGCCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
CCAGCCTAGCCAGTTTCTCACCTGGGTTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCCAAGGGGCCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC
TCTACCCCCAGGGCAGCATCTCAGCTTCGGAACCCTGGGCTGTTTCCTTAGTCTTCATTTTA
TAAAAGTTGTTGCCTTTTTTAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT
ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAAGTCTGTCTTCCCCACCTGCCTAGC
CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAA
AAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

[illegible][illegible]

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSF LTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTTCAAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGATTTTCGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTTCAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTT**TAA**

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTTCGAGGTATATTGTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
CTGGCGGGCCCGCAACACTCCGTCTCACCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
TGTTTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTGCTGGGCCCTACTATGT
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCAGTGGTGCTGGTGG
CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
GGGAGTTCCTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
CCTCAGGGGTAAAAGCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG
ACTGCTGACGGCTGGTCCTGAGGAAGGACAAACTGCCCAGACTTGAGCCCAATTAAATTTTA
TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATCCCCAGTCCC
CTGCACCCCTTCCTGGGACACT**ATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGT
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
CCTTCTCCTGGCTGTTTATTTTATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCAT**TAA**ATTCCTTCTCAGATACCA
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG
GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA
TATTTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
L FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible][illegible]

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTTLSSEE
LPQIFTSLSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG
GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATA
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
GGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTTTAGTATAGCATTTTTTAAAAAATA
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217